

[illegible]

(ii) TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods

(iv) CORRESPONDENCE ADDRESS:  
 (A) ADDRESSEE: DNAX Research Institute  
 (B) STREET: 901 California Avenue  
 (C) CITY: Palo Alto  
 (D) STATE: California  
 (E) COUNTRY: USA  
 (F) ZIP: 94304-1104

(vi) CURRENT APPLICATION DATA:  
 (A) APPLICATION NUMBER: US  
 (B) FILING DATE: 08-MAR-1999  
 (C) CLASSIFICATION:

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (650)852-9196  
(B) TELEFAX: (650)496-1200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 132..1064

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 567  
(D) OTHER INFORMATION: /note= "nucleotides 567, 573, 1336, 1342, and 1369 designated C, but each may be A, C, G, or T"

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 643  
(D) OTHER INFORMATION: /note= "nucleotides 643, 1287, and 1290 designated C, but each may be C or G"

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 772  
(D) OTHER INFORMATION: /note= "nucleotides 772, 806, and 1261 designated G, but each may be A or G"

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1236  
(D) OTHER INFORMATION: /note= "nucleotides 1236, 1260, 1282, and 1289 are designated T, but each may be G or T"

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1247  
(D) OTHER INFORMATION: /note= "nucleotides 1247, 1257, 1293, and 1302 designated C, but each may be C or T"

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1266  
(D) OTHER INFORMATION: /note= "nucleotides 1266 and 1298 designated T, but each may be A or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCGACCCACG CGTCCGCGCT GCGACTCAGA CCTCAGCTCC AACATATGCA TTCTGAAGAA	60
AGATGGCTGA GATGGACAGA ATGCTTTATT TTGGAAAGAA ACAATGTTCT AGGTCAAAC	120
GAGTCTACCA A ATG CAG ACT TTC ACA ATG GTT CTA GAA GAA ATC TGG ACA	170
Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr	
1 5 10	
AGT CTT TTC ATG TGG TTT TTC TAC GCA TTG ATT CCA TGT TTG CTC ACA	218
Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr	
15 20 25	







(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..694

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 193

(D) OTHER INFORMATION: /note= "nucleotide 193 designated  
C, may be C or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

C	CGG	GTC	GAC	CCA	CGC	GTC	CGC	CTG	GTT	TCC	CCC	TGG	CTG	ACA	GTG	46
	Arg	Val	Asp	Pro	Arg	Val	Arg	Leu	Val	Ser	Pro	Trp	Leu	Thr	Val	
	1				5					10					15	
CCT	TGG	TTC	CTG	TCC	TGT	TGG	AAT	GTT	ACC	ATT	GGG	CCT	CCT	GAG	AGC	94
Pro	Trp	Phe	Leu	Ser	Cys	Trp	Asn	Val	Thr	Ile	Gly	Pro	Pro	Glu	Ser	
			20						25					30		
ATC	TGG	GTG	ACG	CCG	GGA	GAA	GCC	TCC	CTC	ATC	ATC	AGG	TTC	TCC	TCT	142
Ile	Trp	Val	Thr	Pro	Gly	Glu	Ala	Ser	Leu	Ile	Ile	Arg	Phe	Ser	Ser	
			35					40					45			
CCC	TTC	GAC	GTC	CCT	CCC	AAC	CTG	GGC	TAT	TTC	CAG	TAC	TAT	GTC	CAT	190
Pro	Phe	Asp	Val	Pro	Pro	Asn	Leu	Gly	Tyr	Phe	Gln	Tyr	Tyr	Val	His	
		50					55					60				
TAC	TGG	GAA	AAG	GCG	GGA	ATC	CAA	AAG	GTT	AAA	GGT	CCT	TTC	AAG	AGC	238
Tyr	Trp	Glu	Lys	Ala	Gly	Ile	Gln	Lys	Val	Lys	Gly	Pro	Phe	Lys	Ser	
	65					70					75					
AAC	TCC	ATC	GTG	TTG	GAT	GGC	TTG	AGA	CCC	TTA	AGA	GAA	TAC	TGT	TTA	286
Asn	Ser	Ile	Val	Leu	Asp	Gly	Leu	Arg	Pro	Leu	Arg	Glu	Tyr	Cys	Leu	
	80				85				90					95		
CAA	GTG	AAG	GCG	CAT	CTC	TTT	CGC	ACA	TCC	TGC	AAC	ACC	TCT	AGG	CCC	334
Gln	Val	Lys	Ala	His	Leu	Phe	Arg	Thr	Ser	Cys	Asn	Thr	Ser	Arg	Pro	
			100					105					110			
GGC	CGC	TTA	AGC	AAC	ATA	ACT	TGC	TAC	GAA	ACA	ATG	ATG	GAT	GCC	ACT	382
Gly	Arg	Leu	Ser	Asn	Ile	Thr	Cys	Tyr	Glu	Thr	Met	Met	Asp	Ala	Thr	
		115						120					125			
ACG	AAG	CTT	CAA	CAA	GTC	ATC	CTC	ATC	GCC	GTG	GGA	GTC	TTT	CTG	TCG	430
Thr	Lys	Leu	Gln	Gln	Val	Ile	Leu	Ile	Ala	Val	Gly	Val	Phe	Leu	Ser	
		130					135					140				
CTG	GCG	GCG	CTG	GCG	GGG	GGC	TGT	TTC	TTC	CTG	GTG	CTG	AGA	TAC	AAA	478
Leu	Ala	Ala	Leu	Ala	Gly	Gly	Cys	Phe	Phe	Leu	Val	Leu	Arg	Tyr	Lys	

155

GGC CTG GTG AAA TAC TGG TTT CAC TCT CCG CCA AGC ATC CCA TCA CAA 526  
 Gly Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln  
 160 165 170 175

ATC GAA GAG TAT CTG AAG GAC CCG AGC CAG CCT ATC CTA GAG GCC CTG 574  
Ile Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu  
180 185 190

GAC AAG GAC ACG TCA CCA ACA GAT GAT GCC TGG GAC TTG GTG TCT GTT 622  
Asp Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val  
195 200 205

GTT GCA TTT CCA GCA AAG GAG CAA GAA GAT GTT CCC CAA AGC ACT TTG 670  
Val Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu  
210 215 220

ACC CAA AAC TCT GGT GCG GTC TGC TAGCCTGTGG GGTAAGGGCT CTGAGCCGAG 724  
Thr Gln Asn Ser Gly Ala Val Cys  
225 230

GAAGCTGCTG ATGTCCATGT CAGCACTTTA TGAATCCGG TCCTCCATTT TCCTGTCCCC 784

AAAAGGCCCG TCAGTGCCTG TGAAGATGTA ACGGGTCTCA TGGGGGCGAC AAGCTTATTG 844

ATTTTTTCT TCAAATAAG AGTTTTCTAA TCATACGCGT TTTTAGAATA ATTCTACAGA 904

TATGTCCCCG AAAGATTAAG ATTTCTCTTA AACACTAAAA AGACATGTAA TTATTTGTTA 964

GCAAATGGGC GTCTGGCACG CCTCTGACAC TTTTTCGTCA GCAGCCAGGA CACGAGGTCC 1024

CCTCCTTGAT GAAGCCCCTC GGGCAGACCA TGTCACCTGT CCCAGCCTGC CCCAAGAAGG 1084

GACATTAAGT GGCCCTTCTT CATATCCAAA CACCTGGCTT GAAATGTGAT TAGCCCTGTA 1144

AATAGTTTCA CAGAGATTAA GCCTTTTTTT CCCCCAAGTT AGGAATAAAA GACTATAATT 1204

AACTTTTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1244

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro  
1 5 10 15

Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile  
                   20                                  25                                  30

Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro  
                   35                                  40                                  45

Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Tyr  
                   50                                  55                                  60

Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn  
                   65                                  70                                  75                                  80

Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln  
                                   85                                  90                                  95

Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly  
                   100                                  105                                  110

Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr  
                   115                                  120                                  125

Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu  
                   130                                  135                                  140

Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly  
                   145                                  150                                  155                                  160

Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile  
                                   165                                  170                                  175

Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp  
                   180                                  185                                  190

Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val  
                   195                                  200                                  205

Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr  
                   210                                  215                                  220

Gln Asn Ser Gly Ala Val Cys  
                   225                                  230

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



[illegible]

Met	Arg	Pro	Thr	Leu	Leu	Trp	Ser	Leu	Leu	Leu	Leu	Gly	Val	Phe		
1				5				10					15			
Ala	Ala	Ala	Ala	Ala	Ala	Pro	Pro	Asp	Pro	Leu	Ser	Gln	Leu	Pro	Ala	
			20					25					30			
Pro	Gln	His	Pro	Lys	Ile	Arg	Leu	Tyr	Asn	Ala	Glu	Gln	Val	Leu	Ser	
		35					40					45				
Trp	Glu	Pro	Val	Ala	Leu	Ser	Asn	Ser	Thr	Arg	Pro	Val	Val	Tyr	Arg	
	50					55					60					
Val	Gln	Phe	Lys	Tyr	Thr	Asp	Ser	Lys	Trp	Phe	Thr	Ala	Asp	Ile	Met	
65				70						75					80	
Ser	Ile	Gly	Val	Asn	Cys	Thr	Gln	Ile	Thr	Ala	Thr	Glu	Cys	Asp	Phe	
				85					90					95		
Thr	Ala	Ala	Ser	Pro	Ser	Ala	Gly	Phe	Pro	Met	Asp	Phe	Asn	Val	Thr	
			100					105					110			
Leu	Arg	Leu	Arg	Ala	Glu	Leu	Gly	Ala	Leu	His	Ser	Ala	Trp	Val	Thr	
		115					120					125				
Met	Pro	Trp	Phe	Gln	His	Tyr	Arg	Asn	Val	Thr	Val	Gly	Pro	Pro	Glu	
	130					135					140					
Asn	Ile	Glu	Val	Thr	Pro	Gly	Glu	Gly	Ser	Leu	Ile	Ile	Arg	Phe	Ser	
145					150					155					160	
Ser	Pro	Phe	Asp	Ile	Ala	Asp	Thr	Ser	Thr	Ala	Phe	Phe	Cys	Tyr	Tyr	
				165					170					175		
Val	His	Tyr	Trp	Glu	Lys	Gly	Gly	Ile	Gln	Gln	Val	Lys	Gly	Pro	Phe	
			180					185					190			
Arg	Ser	Asn	Ser	Ile	Ser	Leu	Asp	Asn	Leu	Lys	Pro	Ser	Arg	Val	Tyr	
		195					200					205				
Cys	Leu	Gln	Val	Gln	Ala	Gln	Leu	Leu	Trp	Asn	Lys	Ser	Asn	Ile	Phe	
	210					215					220					
Arg	Val	Gly	His	Leu	Ser	Asn	Ile	Ser	Cys	Tyr	Glu	Thr	Met	Ala	Asp	
225				230						235					240	
Ala	Ser	Thr	Glu	Leu	Gln	Gln	Val	Ile	Leu	Ile	Ser	Val	Gly	Thr	Phe	
				245					250					255		
Ser	Leu	Leu	Ser	Val	Leu	Ala	Gly	Ala	Cys	Phe	Phe	Leu	Val	Leu	Lys	
			260					265					270			



Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr  
 130 135 140  
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys  
 145 150 155 160  
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu  
 165 170 175  
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg  
 180 185 190  
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val  
 195 200 205  
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Trp Met Val Ala  
 210 215 220  
 Val Ile Leu Met Ala Ser Val Phe Met Val Cys Leu Ala Leu Leu Gly  
 225 230 235 240  
 Cys Phe Ser Leu Leu Trp Cys Val Tyr Lys Lys Thr Lys Tyr Ala Phe  
 245 250 255  
 Ser Pro Arg Asn Ser Leu Pro Gln His Leu Lys Glu Phe Leu Gly His  
 260 265 270  
 Pro His His Asn Thr Leu Leu Phe Phe Ser Phe Pro Leu Ser Asp Glu  
 275 280 285  
 Asn Asp Val Phe Asp Lys Leu Ser Val Ile Ala Glu Asp Ser Glu Ser  
 290 295 300  
 Gly Lys Gln Asn Pro Gly Asp Ser Cys Ser Leu Gly Thr Pro Pro Gly  
 305 310 315 320  
 Gln Gly Pro Gln Ser  
 325

005540 030599